

## Supplementary material

### S1. Calculation of soil water variables

Climate variables and parameters interact and combine with each other and with the soil to generate the environment which the plant grows in, and water becomes available to the plant through soil moisture (Schulze et al. 2007). The variables, days of year with severe soil water stress (SWS) and plant available water (PAW), are used to test whether there is a relationship with syconium size. Days of year with severe soil water stress (SWS) indicates the number of days per year at which soil water content would be at critical plant stress. Severe soil water stress refers to the soil water content at which total evaporation is reduced to below 20% of the maximum evaporation:  $\theta < 0.2 E/E_m$ . With  $\theta$  as the actual soil water content,  $E$  is the total evaporation of a plant/soil system and  $E_m$  is the maximum evaporation that could take place. Plant available water (PAW) is the water in the soil profile that is readily available to plants. In this case  $PAW = \theta_{DUL} - \theta_{PWP}$ . With PAW as the plant available water,  $\theta_{DUL}$  as the drained upper limit of soil water, and  $\theta_{PWP}$  as the permanent wilting point of soil water. The plant available water indicates the storage of water available, and therefore it depends on the soil texture and the soil profile depth and the geological formations (Schulze 2007). The centre-west parts of South Africa have low plant available water and mostly at less than 40 mm deep (Schulze & Horan 2007).

### S2. MCMCglms

Growth form was treated as a multinomial variable with  $J - 1$  linear predictors with  $J$  categories (Hadfield 2010). The priors passed to the Markov chain Monte Carlo generalised linear mixed model (MCMCglmm) take three parts that specify the  $R$ -structure,  $G$ -structure, and fixed effects (Hadfield 2010). The term  $G$  is used to describe a covariance matrix of the random effects, and  $R$  as the covariance matrix of the residual variances that are assumed to follow an inverse-Wishart distribution. The  $R$ - and  $G$ -structures use the scalar parameters  $V$  and  $nu$  to describe the inverse-Wishart distribution. A third parameter, *fix*, can be specified (i.e. a *fixed* variance component is not estimated) so that the model is free to estimate the other variance components. To test and compare the phylogenetic dependencies of each phenotype, we fixed priors for the  $R$ - and  $G$ -structure (as either 0.95 or 0.05 of phenotype variance) using an intercept model (with no fixed factors). By conditioning the variance structure of the model in this way to favour either the phylogeny or the residual component, we compared the respective contributions of each component to phenotypic variation. The deviance information criterion (DIC) was used to compare model fit. The DIC is conceptually similar to the Akaike Information Criterion, with lower values indicating better model fit (Spiegelhalter et al. 2002). The Markov chains of the intercept models were run for  $5.0 \times 10^6$  iterations with a burnin of 10 000 and a thinning interval of 1 000.

## Supplementary Table S1

*Ficus* species used in the canonical outlying mean index (OMI) analyses

Taxon	<i>n</i>	OMI code
<i>Ficus abutilifolia</i>	91	1
<i>Ficus bizanae</i>	15	2
<i>Ficus bubu</i>	5	3
<i>Ficus burkei</i>	56	4
<i>Ficus burtt-davyi</i>	51	5
<i>Ficus cordata</i>	10	6
<i>Ficus cordata</i> subsp. <i>cordata</i>	61	7
<i>Ficus craterostoma</i>	102	8
<i>Ficus glumosa</i>	83	9
<i>Ficus ilicina</i>	17	10
<i>Ficus ingens</i>	117	11
<i>Ficus lingua</i>	4	12
<i>Ficus lutea</i>	22	13
<i>Ficus natalensis</i>	40	14
<i>Ficus natalensis</i> subsp. <i>graniticola</i>	20	15
<i>Ficus petersii</i>	13	16
<i>Ficus polita</i>	5	17
<i>Ficus polita</i> subsp. <i>polita</i>	7	18
<i>Ficus salicifolia</i>	72	19
<i>Ficus sansibarica</i>	7	20
<i>Ficus sansibarica</i> subsp. <i>sansibarica</i>	16	21
<i>Ficus stuhlmannii</i>	31	22
<i>Ficus sur</i>	131	23
<i>Ficus sycomorus</i>	20	24
<i>Ficus sycomorus</i> subsp. <i>gnaphalocarpa</i>	1	25
<i>Ficus sycomorus</i> subsp. <i>sycomorus</i>	41	26
<i>Ficus tettensis</i>	21	27
<i>Ficus thonningii</i>	123	28
<i>Ficus tremula</i>	3	29
<i>Ficus tremula</i> subsp. <i>tremula</i>	4	30
<i>Ficus trichopoda</i>	18	31

## Supplementary Table S2

Growth form categories used to model *Ficus* species in the MCMCglmm analyses; 1 = lithophyte, 2 = tree, 3 = hemi-epiphyte, 4 = lithophyte-hemi-epiphyte, 5 = hemi-epiphyte-tree, 6 = lithophyte-tree, 7 = all forms

	Lithophyte	Hemi-epiphyte	Tree	Code
<i>F. abutilifolia</i>	1	-	-	1
<i>F. bizanae</i>	1	2	-	4
<i>F. bubu</i>	1	2	3	7
<i>F. burkei</i>	1	2	3	7
<i>F. burtt-davyi</i>	1	2	3	7
<i>F. cordata</i>	1	-	-	1
<i>F. cordata</i> subsp. <i>cordata</i>	1	-	-	1
<i>F. craterostoma</i>	1	2	-	4
<i>F. glumosa</i>	1	-	3	6
<i>F. ilicina</i>	1	-	-	1
<i>F. ingens</i>	1	-	3	6
<i>F. lingua</i>	-	2	-	3
<i>F. lutea</i>	-	2	3	5
<i>F. natalensis</i>	1	2	3	7
<i>F. natalensis</i> subsp. <i>natalensis</i>	1	2	3	7
<i>F. petersii</i>	-	2	3	5
<i>F. polita</i>	1	2	3	7
<i>F. polita</i> subsp. <i>polita</i>	1	2	3	7
<i>F. salicifolia</i>	1	-	3	1
<i>F. sansibarica</i>	-	2	-	3
<i>F. sansibarica</i> subsp. <i>sansibarica</i>	-	2	-	3
<i>F. stuhlmannii</i>	-	2	3	5
<i>F. sur</i>	-	-	3	2
<i>F. sycomorus</i>	-	-	3	2
<i>F. sycomorus</i> subsp. <i>gnaphalocarpa</i>	-	-	3	2
<i>F. sycomorus</i> subsp. <i>sycomorus</i>	-	-	3	2
<i>F. tettensis</i>	1	-	-	1
<i>F. tremula</i>	-	2	3	5
<i>F. tremula</i> subsp. <i>tremula</i>	-	2	3	5
<i>F. thonningii</i>	-	2	3	5
<i>F. trichopoda</i>	-	-	3	2

## Supplementary Table S3

The posterior distributions of MCMCglmm coefficients of mean syconium size and growth form responses explained by within- and between-species variance. CI = 95% credible interval. The term  $G$  describes a covariance matrix of the random effects and  $R$  as the covariance matrix of the residual variances. The Bayesian  $p$ -value ( $pMCMC$ ) is  $(2 \times)$  the proportion of values from the posterior estimate that are of the opposite sign to the parameter calculated from the Monte Carlo sampling and provides a way to assess variable support.

	Variable	Posterior mean	Lower CI	Upper CI	Effective sample	$pMCMC$
<i>Syconium size</i>						
G-structure	Phylogeny	1.040	0.335	1.962	1146	-
	Taxon	0.015	0.000	0.059	990	-
R-structure	Residual	0.030	0.020	0.039	990	-
	Species mean PAW	-1.051	-1.758	-0.237	844	<b>0.008</b>
	Within-species PAW	0.002	-0.136	0.135	1106	0.980
	Species mean SWS	-0.834	-1.607	-0.072	990	<b>0.046</b>
	Within-species SWS	-0.005	-0.235	0.250	990	0.962
	<i>Growth form</i>					
G-structure	Phylogeny	1.025	0.941	1.116	2095	-
	Taxon	1.036	0.946	1.134	1980	-
R-structure	Residual	200	200	200	0*	-
	Species mean PAW	273.9	219.5	324.8	319	<b>&lt;0.001</b>
	Within-species PAW	0.000	-4.071	4.154	1980	0.991
	Species mean SWS	-233.6	-276.0	-192.0	317	<b>&lt;0.001</b>
	Within-species SWS	0.047	-7.830	7.370	1980	0.996

\*Fixed prior for categorical response

## Supplementary Table S4

Intercept models showing the 95% highest posterior density intervals of the distribution of the variance for mean syconium size and growth form responses. The term *G* describes a covariance matrix of the random effects, and *R* as the covariance matrix of the residual variances. The table shows models with different prior R- and G-structure variance prior assumptions (as either 0.95 or 0.05 of phenotype variance respectively). CI = Credible Interval; DIC = Deviance Information Criterion

Variance component	Variance prior	Factor	Posterior mean	Lower CI	Upper CI	Effective sample	DIC
<i>Syconium size</i>							
G-structure	0.05	Tree	252.40	120.40	394.90	990	-739.24
		Taxon	0.83	0.21	1.76	990	
R-structure	0.95	Null	0.08	0.08	0.09	990	
G-structure	0.95	Tree	240.40	87.37	424.70	990	-4292.76
		Taxon	11.48	3.85	21.44	990	
R-structure	0.05	Null	0.00	0.00	0.00	990	
<i>Growth form</i>							
G-structure	0.05	Tree	2.85	0.00	6.63	590	3090.20
		Taxon	8.54	4.57	13.22	568	
R-structure	0.95	Null	4.70	4.70	4.70	*0	
G-structure	0.95	Tree	55.85	16.01	90.13	19	3365.89
		Taxon	13.24	0.57	30.02	14	
R-structure	0.05	Null	0.25	0.25	0.25	*0	

\*Fixed variance prior for categorical response.

## Supplementary Table S5

The posterior distribution of the MCMCglmm coefficients for growth form and mean syconium size responses as explained by geobiological variables (biome, aspect, slope), PAW (plant available water), SWS (soil water stress), and phylogeny. CI = 95% credible interval. A relatively high effective sample indicates that the model is mixing well. Strong effects indicated with bold *pMCMC* value. The term *G* describes a covariance matrix of the random effects, and *R* as the covariance matrix of the residual variances

	Variable	Posterior mean	Lower CI	Upper CI	Effective sample	<i>pMCMC</i>	DIC
<i>Syconium size</i>							
G-structure	Phylogeny	2.088	0.931	3.546	990		9117.48
	Taxon	0.008	0.000	0.026	990		
	Biome	0.006	0.000	0.021	990		
	Aspect	0.002	0.000	0.005	990		
R-structure	Residual	0.030	0.020	0.039	961.6		
Fixed effects	PAW	-0.033	-0.159	0.109	990	0.620	
	SWS	-0.072	-0.339	0.187	990	0.606	
	Elevation	0.002	-0.126	0.154	990	0.976	
	Slope	-0.048	-0.215	0.155	990	0.616	
<i>Growth form</i>							
G-structure	Phylogeny	1.083	0.989	1.183	990		735.88
	Taxon	1.144	1.049	1.261	990		
	Biome	1.011	0.920	1.090	896.1		
	Aspect	1.000	0.916	1.095	990		
R-structure	Residual	200	200	200	0		
Fixed effects	PAW	2.540	0.517	4.575	818.5	<b>0.014</b>	
	SWS	-13.174	-15.772	-10.532	1127.8	<b>&lt; 0.001</b>	
	Elevation	-2.288	-4.217	-0.089	1087.3	<b>0.040</b>	
	Slope	2.587	0.309	4.884	990	<b>0.034</b>	

## References (Supplementary material)

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